

## New Tools for Monitoring and Predicting Harmful Algal Blooms

Sonya T. Dyhrman  
Woods Hole Oceanographic Institution  
Biology Department MS#32  
(508) 289-3608  
sdyhrman@whoi.edu

**Authors:** Sonya T. Dyhrman, Donald M. Anderson, Deana Erdner and Sheean T. Haley

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Harmful algal blooms (HABs) are the proliferation of algae that can have a deleterious impact on human health and the coastal marine environment. For example, some algae produce dangerous neurotoxins that can accumulate in the food web and be transferred to humans or marine mammals.

Even at low densities, some harmful algae, such as the toxin-producing dinoflagellate *Alexandrium fundyense*, can result in serious health impacts. We have recently developed a molecular method that enables us to quantify the presence of a gene specific to *A. fundyense* in field populations. Gene amplification from a field sample is compared with that of a known sample to generate an estimate of cell abundance. This technique is called quantitative PCR (qPCR) and it offers a rapid, high-throughput method for monitoring toxic blooms of *A. fundyense*. Based on preliminary results, cell densities determined by qPCR have been in the same range as other more time-consuming detection methods.

While bloom detection is imperative, it is also important to understand what factors (such as nutrient availability) influence the initiation, maintenance, and eventual decline of these blooms. From a human health perspective, this is especially necessary so adequate warning can be given to recreational areas and shellfisheries to protect human exposure as well as minimize economic losses. It is widely accepted that nutrients play an important regulatory role in growth, bloom dynamics, and toxin production in harmful algae. We are developing a technique called enzyme labeled fluorescence (ELF) to assess nutrient utilization by harmful algal species. Cellular enzymes can hydrolyze organic nutrients into potentially more bioavailable forms, and are often regulated by the nutritional health of the organism. ELF can identify enzyme activity in individual harmful cells and thus be used as a proxy for assessing the nutritional status or 'health' of HABs. Our results to date indicate that ELF-based detection of enzyme activity may be possible for many HAB species. Monitoring and identifying changes in nutritional status will improve our ability to predict blooms and understand how coastal eutrophication may influence bloom dynamics.

New tools such as qPCR and ELF show great promise for providing accurate and timely information about field populations of harmful algae. Continued development and application of these methods should offer improved strategies for protecting human health and the environment.